

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/744,852

DATE: 04/25/2001

TIME: 07:30:53

Input Set : A:\es.txt

Output Set: N:\CRF3\04252001\I744852.raw

ENTERED

3 <110> APPLICANT: FROHBERG, Claus
5 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A-AMYLASE, PLANTS WHICH
SYNTHESIZE A
6 MODIFIED STARCH, GENERATION PROCESSES AND USES
8 <130> FILE REFERENCE: 514413-3864
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/744,852
C--> 10 <141> CURRENT FILING DATE: 2001-01-30
10 <150> PRIOR APPLICATION NUMBER: PCT/EP99/05523
11 <151> PRIOR FILING DATE: 1999-07-30
13 <150> PRIOR APPLICATION NUMBER: 198 36 099.1
14 <151> PRIOR FILING DATE: 1998-07-31
16 <160> NUMBER OF SEQ ID NOS: 2
18 <170> SOFTWARE: PatentIn version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1950
22 <212> TYPE: DNA
23 <213> ORGANISM: Solanum tuberosum
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (16)..(1752)
28 <223> OTHER INFORMATION: coding sequence beta-amylase
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32 attaataatta ttatt atg gca atg agt ctg cca cac cag atc ggt gcc tta 51
33 Met Ala Met Ser Leu Pro His Gln Ile Gly Ala Leu
34 1 5 10
36 tca gga aca tcg ctc acg gcg gaa acc ggt gga gtt tca tgc gaa gtt 99
37 Ser Gly Thr Ser Leu Thr Ala Glu Thr Gly Gly Val Ser Cys Glu Val
38 15 20 25
40 ccg gcg aag ggg agt tca gct aca tca gct atg tgg aga aca ccg atg 147
41 Pro Ala Lys Gly Ser Ser Ala Thr Ser Ala Met Trp Arg Thr Pro Met
42 30 35 40
44 acg aat tta aaa gta tcg gta caa aaa aca gga act gaa att gac agg 195
45 Thr Asn Leu Lys Val Ser Val Gln Lys Thr Gly Thr Glu Ile Asp Arg
46 45 50 55 60
48 gtg tcg ccg tcg ccg tcg ccg ccg atg agt ccg atg atg gga gga gga 243
49 Val Ser Pro Ser Pro Ser Pro Pro Met Ser Pro Met Met Gly Gly Gly
50 65 70 75
52 atg cgg ccg gat tta tta gcg tgt caa gcg ttg atg gaa gct cag gta 291
53 Met Arg Pro Asp Leu Leu Ala Cys Gln Ala Leu Met Glu Ala Gln Val
54 80 85 90
56 gat gag gta gtt gag aga gaa tat aag gtt agg aat tcg tcg gag aaa 339
57 Asp Glu Val Val Glu Arg Glu Tyr Lys Val Arg Asn Ser Ser Glu Lys
58 95 100 105
60 gag aaa gga gtt ccg gtg ttt gtt atg atg ccg ttg gat agt gtg aaa 387
61 Glu Lys Gly Val Pro Val Phe Val Met Met Pro Leu Asp Ser Val Lys
62 110 115 120
64 atg gat cat act gtg aat agg aag aag gcg atg aat gcg agt tta cag 435
65 Met Asp His Thr Val Asn Arg Lys Lys Ala Met Asn Ala Ser Leu Gln

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66	125					130				135					140		
68	gcg	ttg	aag	agc	gcc	ggt	gtg	gaa	ggg	att	atg	atg	gat	gtg	tgg	tgg	483
69	Ala	Leu	Lys	Ser	Ala	Gly	Val	Glu	Gly	Ile	Met	Met	Asp	Val	Trp	Trp	
70					145					150					155		
72	gga	ttg	gtg	gag	aga	gat	gcg	ccg	gga	gag	tat	aat	tgg	ggc	ggt	tat	531
73	Gly	Leu	Val	Glu	Arg	Asp	Ala	Pro	Gly	Glu	Tyr	Asn	Trp	Gly	Gly	Tyr	
74					160					165					170		
76	gct	gag	ctt	atg	gaa	atg	gcg	aaa	aaa	cat	gga	ctc	aaa	ggt	caa	gct	579
77	Ala	Glu	Leu	Met	Glu	Met	Ala	Lys	Lys	His	Gly	Leu	Lys	Val	Gln	Ala	
78					175					180					185		
80	gtg	atg	tct	ttc	cat	caa	tgt	ggt	gga	aac	gtc	ggt	gat	tcc	tgc	acg	627
81	Val	Met	Ser	Phe	His	Gln	Cys	Gly	Gly	Asn	Val	Gly	Asp	Ser	Cys	Thr	
82		190					195					200					
84	atc	cct	ctt	cca	agg	tgg	gtt	gtt	gag	gag	atg	gag	aag	gat	cca	gat	675
85	Ile	Pro	Leu	Pro	Arg	Trp	Val	Val	Glu	Glu	Met	Glu	Lys	Asp	Pro	Asp	
86	205					210					215					220	
88	ctt	gca	tac	aca	gat	cag	tgg	gga	agg	agg	aat	ttt	gaa	tat	gta	tcg	723
89	Leu	Ala	Tyr	Thr	Asp	Gln	Trp	Gly	Arg	Arg	Asn	Phe	Glu	Tyr	Val	Ser	
90					225					230					235		
92	ctt	ggt	tgc	gat	aca	ctt	cca	gtt	ctt	aaa	gga	agg	act	cct	gtc	caa	771
93	Leu	Gly	Cys	Asp	Thr	Leu	Pro	Val	Leu	Lys	Gly	Arg	Thr	Pro	Val	Gln	
94					240					245					250		
96	tgc	tat	tct	gat	ttc	atg	aga	ggg	ttt	aga	gat	aga	ttt	gag	aat	ctc	819
97	Cys	Tyr	Ser	Asp	Phe	Met	Arg	Gly	Phe	Arg	Asp	Arg	Phe	Glu	Asn	Leu	
98					255				260					265			
100	cta	ggt	gac	acc	att	gtg	gaa	att	caa	gtc	ggg	atg	ggt	cca	gct	gga	867
101	Leu	Gly	Asp	Thr	Ile	Val	Glu	Ile	Gln	Val	Gly	Met	Gly	Pro	Ala	Gly	
102																	
104	gag	ctc	cgt	tat	cca	tcc	tat	ccg	gaa	aaa	gat	gga	gta	tgg	aaa	ttc	915
105	Glu	Leu	Arg	Tyr	Pro	Ser	Tyr	Pro	Glu	Lys	Asp	Gly	Val	Trp	Lys	Phe	
106	285					290					295					300	
108	cct	gga	att	ggt	gct	ttt	cag	tgt	tat	gac	aag	tac	atg	atc	agt	agc	963
109	Pro	Gly	Ile	Gly	Ala	Phe	Gln	Cys	Tyr	Asp	Lys	Tyr	Met	Ile	Ser	Ser	
110					305					310					315		
112	tta	cag	ggt	gca	gca	gaa	gct	ttt	ggt	aag	cct	gaa	tgg	gga	cac	acc	1011
113	Leu	Gln	Gly	Ala	Ala	Glu	Ala	Phe	Gly	Lys	Pro	Glu	Trp	Gly	His	Thr	
114					320				</								

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132 gtt aag att gca ggt att cac tgg cac tat gga aca agg tcc cat gcc      1251
133 Val Lys Ile Ala Gly Ile His Trp His Tyr Gly Thr Arg Ser His Ala
134          400          405          410
136 cct gag ctg acc gct gga tac tac aac acc cgt aac cga gat ggt tac      1299
137 Pro Glu Leu Thr Ala Gly Tyr Tyr Asn Thr Arg Asn Arg Asp Gly Tyr
138          415          420          425
140 ctt ccc atc gcc caa atg ctt gcc cgc cac ggt gca gtt ttc aac ttc      1347
141 Leu Pro Ile Ala Gln Met Leu Ala Arg His Gly Ala Val Phe Asn Phe
142          430          435          440
144 aca tgt gtt gag atg cgt gac cac gag cag cca caa gat gca cta tgt      1395
145 Thr Cys Val Glu Met Arg Asp His Glu Gln Pro Gln Asp Ala Leu Cys
146 445          450          455          460
148 gca cct gag aag ttg gtt agg caa gtg gct tta gca act cag gaa gct      1443
149 Ala Pro Glu Lys Leu Val Arg Gln Val Ala Leu Ala Thr Gln Glu Ala
150          465          470          475
152 caa gtt cca ctt gct ggg gag aat gca ttg cca cga tac gat gat tat      1491
153 Gln Val Pro Leu Ala Gly Glu Asn Ala Leu Pro Arg Tyr Asp Asp Tyr
154          480          485          490
156 gca cat gaa cag atc ctt caa gca tcc tca ttg aat atc aac gat caa      1539
157 Ala His Glu Gln Ile Leu Gln Ala Ser Ser Leu Asn Ile Asn Asp Gln
158          495          500          505
160 tca ggt gat aga gag atg tgc gcg ttt aca tat ttg agg atg aat cct      1587
161 Ser Gly Asp Arg Glu Met Cys Ala Phe Thr Tyr Leu Arg Met Asn Pro
162          510          515          520
164 gac cta ttc cat cct gat aac tgg agg cga ttc gtt gcc ttc gtg aag      1635
165 Asp Leu Phe His Pro Asp Asn Trp Arg Arg Phe Val Ala Phe Val Lys
166 525          530          535          540
168 aaa atg aaa gaa gga aaa gac gca aac aaa tgc cgg gaa caa gta gag      1683
169 Lys Met Lys Glu Gly Lys Asp Ala Asn Lys Cys Arg Glu Gln Val Glu
170          545          550          555
172 agg gag gca gag cat ttc gtg cat ata act cag ccg tta gtg caa gaa      1731
173 Arg Glu Ala Glu His Phe Val His Ile Thr Gln Pro Leu Val Gln Glu
174          560          565          570
176 gct gca gct gcc ctc atg cac taagcaaatg gttgtcaaat agtactgtaa      1782
177 Ala Ala Ala Ala Leu Met His
178          575
180 ttttgatcct tttagctaac atggagtttt tcaacatggt acgaggatct tatagctcgt      1842
182 tatcgttctt cttatatggt tgtaaaactg tccatcgtgt attttttcga agttagacat      1902
184 tatgtcttaa tgaaatgata cataattcag tagtaaaaaa aaaaaaaa      1950
187 <210> SEQ ID NO: 2
188 <211> LENGTH: 579
189 <212> TYPE: PRT
190 <213> ORGANISM: Solanum tuberosum
192 <400> SEQUENCE: 2
194 Met Ala Met Ser Leu Pro His Gln Ile Gly Ala Leu Ser Gly Thr Ser
195 1          5          10          15
198 Leu Thr Ala Glu Thr Gly Gly Val Ser Cys Glu Val Pro Ala Lys Gly
199          20          25          30
202 Ser Ser Ala Thr Ser Ala Met Trp Arg Thr Pro Met Thr Asn Leu Lys

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302 Gln Met Leu Ala Arg His Gly Ala Val Phe Asn Phe Thr Cys Val Glu
303           435           440           445
306 Met Arg Asp His Glu Gln Pro Gln Asp Ala Leu Cys Ala Pro Glu Lys
307           450           455           460
310 Leu Val Arg Gln Val Ala Leu Ala Thr Gln Glu Ala Gln Val Pro Leu
311 465           470           475           480
314 Ala Gly Glu Asn Ala Leu Pro Arg Tyr Asp Asp Tyr Ala His Glu Gln
315           485           490           495
318 Ile Leu Gln Ala Ser Ser Leu Asn Ile Asn Asp Gln Ser Gly Asp Arg
319           500           505           510
322 Glu Met Cys Ala Phe Thr Tyr Leu Arg Met Asn Pro Asp Leu Phe His
323           515           520           525
326 Pro Asp Asn Trp Arg Arg Phe Val Ala Phe Val Lys Lys Met Lys Glu
327           530           535           540
330 Gly Lys Asp Ala Asn Lys Cys Arg Glu Gln Val Glu Arg Glu Ala Glu
331 545           550           555           560
334 His Phe Val His Ile Thr Gln Pro Leu Val Gln Glu Ala Ala Ala Ala
335           565           570           575
338 Leu Met His

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date